and *Trichuris trichuria* in all school.

Conclusion: Helminths is a public health problem in Kisumu municipality with *S.mansoni* being the commonest. Geographical mapping proved an important tool, it provides accurate information that allows good planning and implementation of mass drug administration through schools. These results provide current epidemiologic information to the Ministry of Health and stakeholders that could be used in targeted implementation of helminths control and eradication strategies.

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Further characterization of the metabolome of *Mycobacterium tuberculosis*

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Background: Due to high incidence rates and the development of new drug-resistant or multidrug-resistant strains of TB, the development of new medicines and treatments is a necessity. In order to develop these drugs, *Mycobacterium tuberculosis* (Mtb) needs to be studied more completely; this study performs a characterization of the metabolome of *Mtb.* A previous project used comparative genomics to identify genes unique to pathogens and to *M. tuberculosis*. Many of the interesting genes that emerged were annotated as uncharacterised or hypothetical proteins.

Methods & Materials: To unravel their roles in the cell, data has been integrated from a variety of sources, both computationally predicted and experimental, to generate functional networks for the proteome. This first step involved creating a catalog of *Mtb* metabolic pathways and their phylogenetic profiles. The data from multiple resources was compiled together into a matrix of all *Mtb* strain H37Rv proteins, along with unique (non-orthologous) proteins from strains KZN 1435, CDC1551, H37Ra and F11. Each protein shows a full phylogenetic profile of all organisms with orthologs in *Mtb*. Pathway data was initially filled in from KEGG and UniPathway data, and then additional uncharacterized pathways were predicted using Gene Ontology (GO) terms, KEGG reference pathways and homology to characterized proteins from closely related organisms. Next these functional networks were used in an attempt to find 'missing' reactions in the pathways. Following this, pathway information has been compared between *Mtb* and *M.leprae, E. coli*, and the reference pathways.

Results: Some pathways have missing steps in cases where Mtb uses the host metabolism, and significant pathways in this regard have been found and imaged on pathway maps. Significant differences between the compared species could show copies or missing pathways in *Mtb.* In the end, the number of proteins with unclassified pathway involvement could be split into different categories: possible metabolic proteins with either vague descriptions or the exact enzyme known, classified non-metabolic proteins and unclassified proteins. A number of interesting pathways that could be completed or almost completed were located.

development

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Clinical outcome of nontuberculous mycobacterial active disease in non-HIV patients at a Brazilian reference center

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Background: Nontuberculous mycobacterial (NTM) infections are an emerging challenge in terms of diagnosis, surveillance and treatment. Objectives: to evaluate the relative frequency and clinical outcome of active nontuberculous mycobacterial cases among non-HIV patients in a Brazilian reference center.

Methods & Materials: A retrospective, longitudinal and descriptive study was performed involving patients non-HIV adults patients followed in a Regional Reference Center for Mycobacteria in Brazilian Southest area, from 2006 to 2013. ATS criteria (2007) were employed for the diagnosis and treatment. BACTEC MGIT and PRA (PCR restriction analysis) were used for detection and species identification, respectively.

Results: Thirty one cases of active disease caused by nontuberculous mycobacterial (NTM) were followed. The relative frequency according to species was the following: *M. avium* in 10 (32.2%), *M. kansasii* in 8 (25.8%), *M. abscessus* in 7 (22.5%), *M. chelonae* in3 (9.6%), *M. fortuitum* in one case, and others in 2 (6.4%) cases. Pulmonary (exclusively) site was the most common in 25 (80.6%) patients, followed by extra-pulmonary in 4 (12.9%) and pulmonary associated to extra-pulmonary in 2 (6.4%) cases. Evident predisponent risk factor was observed in 24 (77.4%) cases: underlying lung disease in 14 (58.3%); previous surgery procedure in 4 (16.6%); others in 2(8.3%) cases. The most frequent antimicobacterial regimen was Claritromicin, Amikacin associated to fluorquinolone (Levofloxacin/ofloxacin). Microbiological conversion was observed in a median of 6 months after the beginning of the therapy. Clinical outcome was favorable in 11(35.5%) patients in the 6th month after the start of specific treatment and 14(45.2%) in 12th month. Six patients with *M. abscessus* underwent to multiple treatments with persistence of isolation of NTM.

Conclusion: The relative frequency of NMT species observed was similar as reported by others authors. Patients with pulmonary disease caused by *M. abscessus* had poor outcome with persistant detection. Besides the opportunistic character, these results highlight the necessity of evaluation of new combined regimens including surgery and multiple parenteral antimicrobial for prolonged time in order to deal with nontuberculous mycobacterial.

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